IN THE DRAWINGS:

Please amend the drawings according to the attached set of figures, on which the amendments are indicated in red ink. Specifically, please replace in sequence 3 of Figure 3A amino acids 18H, 36E and 37L with 18R, 36D and 37V, respectively. Also, please replace in sequence 3 of Figure 3B, amino acids 447K and 506Q with 447E and 506E.

The attached replacement sheets, which include Figures 3A and 3B, replace the original sheets of drawings for Figures 3A and 3B.

Attachments following last page of this response:

Replacement Sheets (2 pages)

Annotated Sheets Showing Changes (2 pages)

IN THE SEQUENCE LISTING

Please replace the sequence listing in the above-captioned application with the attached substitute sequence listing. Two CD-R copies of the substitute sequence listing accompany this amendment and response.

REMARKS

Applicant hereby submits enclosures that fulfill the requirements under 37 C.F.R. §§1.821-1.825. Amendments to the specification insert the two CD-R copies of the substitute Sequence Listing and sequence identifiers in the specification. Minor typographical amendments are made to the specification and figures with regard to the sequence listing. No new matter has been added. Attached hereto is a marked-up version of the changes made to the specification by the current amendment. Any fees that may be due in connection with the filing of this paper or with this application may be charged to Deposit Account No. 06-1050. If a Petition for Extension of time is needed, this paper is to be considered such Petition.

The amendment of the paragraph beginning at page 5, line 25 - 31 identifies the nucleotide and amino acid SEQ ID Nos. for AAV-1, AAV-6, AAV-3, AAV-3B, AAV-4, AAV-2 and AAV-5 as being SEQ ID Nos. 736, 737; 738, 739; 740, 741; 742, 743; 744, 745; 746, 747; and 748, 749; respectively. This amendment finds basis, for example, in the substitute sequence listing which adds the respective nucleotide and amino acid sequences for the protein sequences shown in Figures 3A and 3B. The amendment of the paragraph beginning at page 9, line 3-19 replaces the GenBank Accession number for AAV-6 from "NC_001729" to –NC_001862.– NC_001729 is the GenBank Accession number for AAV-3 as identified in the specification on page 9, lines 9 – 10, whereas NC_001862 is the proper GenBank Accession number for AAV-6.

Amendments have been made to Figures 3A and 3B. Specifically, amino acids 18H, 36E, 37L, 447K and 506Q have been corrected to 18R, 36D, 37V, 447E and 506E, respectively. Basis for the amendment is found in the specification, for example, on page 6, line 2 in which sequence 3 of Figures 3A and 3B is identified as being AAV-3. Further basis can be found, for example, at page 9, lines 9 – 10 in which AAV-3 is identified by GenBank Accession No. NC_001729 and ATCC No. VR-681. Red ink markings of the changes to be incorporated are submitted with this amendment for approval by the Examiner. In addition, replacement sheets of drawings are submitted with this amendment.

Attached herewith are two CD-R copies of the substitute sequence listing, and a verified statement that the content of the computer readable copies are the same in accordance with 37 C.F.R §§1.821-1.825. The instant amendment seeks to amend the sequence listing by adding the

inadvertently omitted amino acid sequences listed in Figures 3A and 3B, along with their corresponding nucleotide sequences identified by their GenBank number on page 9, lines 8-14. These sequences have been designated as SEQ ID Nos. 736 – 749 in the substitute sequence listing. The amendment finds basis, for example, at page 6, lines 1 – 3 and page 9, lines 8 – 14 of the specification as well as in Figures 3A and 3B. In addition, items <140> and <141> of the sequence listing are amended to incorporate the now-available U.S. Application Serial number, 10/022,390, and the date on which the above-identified application was filed, December 17, 2001. The two computer-readable copies of the substitute sequence listing are titled 912SEQ.002.txt are identical to each other. The substitute sequence listing contains no new matter. These sequences are entered into the substitute sequence listing provided herewith.

No new matter is added.

* * *

Entry of this amendment and examination of the application are respectfully requested.

Respectfully submitted,

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APPENDIX

FIGURE 3A

```
          10        20        30        40        50        60
1  MPGFYEIVIKVPSDLDEHLPGISDSFVSWVAEKEWELPPDSDMDLNLIEQAPLTVAEKLQ   60
2  MPGFYEIVIKVPSDLDEHLPGISDSFVNWVAEKEWELPPDSDMDLNLIEQAPLTVAEKLQ   60
3  MPGFYEIVLKVPSDLDEHLPGISNSFVNWVAEKEWELPPDSDMDPNLIEQAPLTVAEKLQ   60
4  MPGFYEIVLKVPSDLDEHLPGISNSFVNWVAEKEWELPPDSDMDPNLIEQAPLTVAEKLQ   60
5  MPGFYEIVLKVPSDLDEHLPGISDSFVSWVAEKEWELPPDSDMDLNLIEQAPLTVAEKLQ   60
6  MPGFYEIVIKVPSDLDGHLPGISDSFVNWVAEKEWELPPDSDMDLNLIEQAPLTVAEKLQ   60
7  MATFYEVIVRVPFDVEEHLPGISDSFVDWVTGQIWELPPESDLNLTLVEQPQLTVADRIR   60
C  M**FYE**:*VP*D***HLPGIS+SFV:WV****WELPP*SD**+*L*EQ**LTVA****

          70        80        90       100       110       120
1  RDFLVQWRRVSKAPEALFFVQFEKGESYFHLHILVETTGVKSMVLGRFLSQIRDKLVQTI  120
2  RDFLVQWRRVSKAPEALFFVQFEKGESYFHLHILVETTGVKSMVLGRFLSQIRDKLVQTI  120
3  REFLVEWRRVSKAPEALFFVQFEKGETYFHLHVLIETIGVKSMVVGRYVSQIKEKLVTRI  120
4  REFLVEWRRVSKAPEALFFVQFEKGETYFHLHVLIETIGVKSMVVGRYVSQIKEKLVTRI  120
5  REFLVEWRRVSKAPEALFFVQFEKGDSYFHLHILVETVGVKSMVVGRYVSQIKEKLVTRI  120
6  RDFLTEWRRVSKAPEALFFVQFEKGESYFHMHVLVETTGVKSMVLGRFLSQIREKLIQRI  120
7  RVFLYEWNKFSKQ-ESKFFVQFEKGSEYFHLHTLVETSGISSMVLGRYVSQIRAQLVKVV  119
C  R:FL++W***SK**E**FFVQFEKG+:YFH*H:L+ET:G**SMV:GR::SQI::*L*::*

         130       140       150       160       170       180
1  YRGIEPTLPNWFAVTKTRNGAGGGNKVVDECYIPNYLLPKTQPELQWAWTNMEEYISACL  180
2  YRGIEPTLPNWFAVTKTRNGAGGGNKVVDECYIPNYLLPKTQPELQWAWTNMEEYISACL  180
3  YRGVEPQLPNWFAVTKTRNGAGGGNKVVDDCYIPNYLLPKTQPELQWAWTNMDQYLSACL  180
4  YRGVEPQLPNWFAVTKTRNGAGGGNKVVDDCYIPNYLLPKTQPELQWAWTNMDQYLSACL  180
5  YRGVEPQLPNWFAVTKTRNGAGGGNKVVDDCYIPNYLLPKTQPELQWAWTNMDQYISACL  180
6  YRGIEPTLPNWFAVTKTRNGAGGGNKVVDECYIPNYLLPKTQPELQWAWTNMEQYLSACL  180
7  FQGIEPQINDWVAITKVKK--GGANKVVDSGYIPAYLLPKVQPELQWAWTNLDEYKLAAL  177
C  **G:EP:***W*A*TK*****GG*NKVVD:*YIP*YLLPK*QPELQWAWTN*::Y:*A*L

         190       200       210       220       230       240
1  NLAERKRLVAQHLTHVSQTQEQNKENLNPNSDAPVIRSKTSARYMELVGWLVDRGITSEK  240
2  NLAERKRLVAHDLTHVSQTQEQNKENLNPNSDAPVIRSKTSARYMELVGWLVDRGITSEK  240
3  NLAERKRLVAQHLTHVSQTQEQNKENQNPNSDAPVIRSKTSARYMELVGWLVDRGITSEK  240
4  NLAERKRLVAQHLTHVSQTQEQNKENQNPNSDAPVIRSKTSARYMELVGWLVDRGITSEK  240
5  NLAERKRLVAQHLTHVSQTQEQNKENQNPNSDAPVIRSKTSARYMELVGWLVDRGITSEK  240
6  NLTERKRLVAQHLTHVSQTQEQNKENQNPNSDAPVIRSKTSARYMELVGWLVDKGITSEK  240
7  NLEERKRLVAQFLAESSQRS-QEAASQREFSADPVIKSKTSQKYMALVNWLVEHGITSEK  236
C  NL+ERKRLVA*+L***SQ***Q****+***S**PVI*SKTS**YM*LV*WLV*+GITSEK

         250       260       270       280       290       300
1  QWIQEDQASYISFNAASNSRSQIKAALDNAGKIMALTKSAPDYLVGPAPPADIKTNRIYR  300
2  QWIQEDQASYISFNAASNSRSQIKAALDNAGKIMALTKSAPDYLVGPAPPADIKTNRIYR  300
3  QWIQEDQASYISFNAASNSRSQIKAALDNASKIMSLTKTAPDYLVGSNPPEDITKNRIYQ  300
4  QWIQEDQASYISFNAASNSRSQIKAALDNASKIMSLTKTAPDYLVGSNPPEDITKNRIYQ  300
5  QWIQEDQASYISFNAASNSRSQIKAALDNASKIMSLTKTAPDYLVGQNPPEDISSNRIYR  300
6  QWIQEDQASYISFNAASNSRSQIKAALDNAGKIMSLTKTAPDYLVGQQPVEDISSNRIYK  300
7  QWIQENQESYLSFNSTGNSRSQIKAALDNATKIMSLTKSAVDYLVGSSVPEDISKNRIWQ  296
C  QWIQE*Q*SY*SFN***NSRSQIKAALDNA:KIM+LTK:A*DYLVG::**+DI::NRI*:

         310       320       330       340       350       360
1  ILELNGYEPAYAGSVFLGWAQKRFGKRNTIWLFGPATTGKTNIAEAIAHAVPFYGCVNWT  360
2  ILELNGYDPAYAGSVFLGWAQKRFGKRNTIWLFGPATTGKTNIAEAIAHAVPFYGCVNWT  360
3  ILELNGYDPQYAASVFLGWAQKKFGKRNTIWLFGPATTGKTNIAEAIAHAVPFYGCVNWT  360
4  ILELNGYDPQYAASVFLGWAQKKFGKRNTIWLFGPATTGKTNIAEAIAHAVPFYGCVNWT  360
5  ILEMNGYDPQYAASVFLGWAQKKFGKRNTIWLFGPATTGKTNIAEAIAHAVPFYGCVNWT  360
6  ILELNGYDPQYAASVFLGWATKKFGKRNTIWLFGPATTGKTNIAEAIAHTVPFYGCVNWT  360
7  IFEMNGYDPAYAGSILYGWCQRSFNKRNTVWLYGPATTGKTNIAEAIAHTVPFYGCVNWT  356
C  I*E+NGY*P:YA:S***GW***:F*KRNT*WL*GPATTGKTNIAEAIAH+VPFYGCVNWT
```

FIGURE 3B

```
          370        380        390        400        410        420
1  NENFPFNDCVDKMVIWWEEGKMTAKVVESAKAILGGSKVRVDQKCKSSAQIDPTPVIVTS  420
2  NENFPFNDCVDKMVIWWEEGKMTAKVVESAKAILGGSKVRVDQKCKSSAQIDPTPVIVTS  420
3  NENFPFNDCVDKMVIWWEEGKMTAKVVESAKAILGGSKVRVDQKCKSSAQIEPTPVIVTS  420
4  NENFPFNDCVDKMVIWWEEGKMTAKVVESAKAILGGSKVRVDQKCKSSAQIEPTPVIVTS  420
5  NENFPFNDCVDKMVIWWEEGKMTAKVVESAKAILGGSKVRVDQKCKSSAQIDPTPVIVTS  420
6  NENFPFNDCVDKMVIWWEEGKMTAKVVESAKAILGGSKVRVDQKCKSSAQIDPTPVIVTS  420
7  NENFPFNDCVDKMLIWWEEGKMTNKVVESAKAILGGSKVRVDQKCKSSVQIDSTPVIVTS  416
C  NENFPFNDCVDKM*IWWEEGKMT*KVVESAKAILGGSKVRVDQKCKSS*QI+**TPVIVTS

          430        440        450        460        470        480
1  NTNMCAVIDGNSTTFEHQQPLQDRMFKFELTRRLEHDFGKVTKQEVKEFFRWAQDHVTEV  480
2  NTNMCAVIDGNSTTFEHQQPLQDRMFKFELTRRLEHDFGKVTKQEVKEFFRWAQDHVTEV  480
3  NTNMCAVIDGNSTTFEHQQPLQDRMFKFELTRRLDHDFGKVTKQEVKDFFRWASDHVTDV  480
4  NTNMCAVIDGNSTTFEHQQPLQDRMFKFELTRRLDHDFGKVTKQEVKDFFRWASDHVTDV  480
5  NTNMCAVIDGNSTTFEHQQPLQDRMFKFELTKRLEHDFGKVTKQEVKDFFRWASDHVTEV  480
6  NTNMCAVIDGNSTTFEHQQPLQDRMFKFELTRRLDHDFGKVTKQEVKDFFRWAKDHVVEV  480
7  NTNMCVVVDGNSTTFEHQQPLEDRMFKFELTKRLPPDFGKITKQEVKDFFAWAKVNQVPV  476
C  NTNMC*V*DGNSTTFEHQQPL*DRMFKFELT+RL:*DFGK*TKQEVK+FF*WA:***+:V

          490        500                                  510        520
1  AHEFYVRKGGANKRPAPDDADKSEPKRA----------------------CPSVADPSTSDAEG  522
2  AHEFYVRKGGANKRPAPDDADKSEPKRA----------------------CPSVADPSTSDAEG  522
3  AHEFYVRKGGAKKRPASNDADVSEPKRQ----------------------CTSLAQPTTSDAEA  522
4  AHEFYVRKGGAKKRPASNDADVSEPKRQ----------------------CTSLAQPTTSDAEA  522
5  THEFYVRKGGARKRPAPNDADISEPKRA----------------------CPSVAQPSTSDAEA  522
6  EHEFYVKKGGAKKRPAPSDADISEPKRV----------------------RESVAQPSTSDAEA  522
7  THEFKVPRELAGTKGAEKSLKRPLGDVTNTSYKSLEKRARLSFVPETPRSSDVTVDPAPL  536
C  :HEF*V+***A:***A::***.*****:                          +:*:*:*:***A*:

          530        540        550        560        570        580
1  APVDFADRYQNKCSRHAGMLQMLFPCKTCERMNQNFNICFTHGTRDCSECFP--GVSESQ  580
2  APVDFADRYQNKCSRHAGMLQMLFPCKTCERMNQNFNICFTHGTRDCSECFP--GVSESQ  580
3  P-ADYADRYQNKCSRHVGMNLMLFPCKTCERMNQISNVCFTHGQRDCGECFPGMSESQPV  581
4  P-ADYADRYQNKCSRHVGMNLMLFPCKTCERMNQISNVCFTHGQRDCGECFPGMSESQPV  581
5  P-VDYADRYQNKCSRHVGMNLMLFPCRQCERMNQNVDICFTHGVMDCAECFP-VSESQPV  580
6  S-INYADRYQNKCSRHVGMNLMLFPCRQCERMNQNSNICFTHGQKDCLECFP--VSESQP  579
7  RPLNWNSRYDCKCDYHAQFDNISNKCDECEYLNRGKNGCICHNVTHCQICHG--------  588
C  :::+:**RY**KC**H:**::****C::CE**N*::*:C**H*::*C.*C**.::+:::

          590        600        610        620
1  PVVRKRTYRKLCAIHHLLGRAPEIACSACDLVNVDLDDCVSEQ                    623
2  PVVRKRTYRKLCAIHHLLGRAPEIACSACDLVNVDLDDCVSEQ                    623
3  SVVKKKTYQKLCPIHHILGRAPEIACSACDLANVDLDDCVSEQ                    624
4  SVVKKKTYQKLCPIHHILGRAPEIACSACDLANVDLDDCVSEQ                    624
5  SVVRKRTYQKLCPIHHIMGRAPEVACSACELANVDLDDCDMEQ                    623
6  VSVVKKAYQKLCYIHHIMG-KVPDACTACDLVNVDLDDCIFEQ                    621
7  ----------------------IPPWEKENLSDFGDFDDANKEQ                    610
C  :+*:*:+*:***:***::*++++:**+**+*:*:D*DD*::EQ
```